

- 33 -

GCTTGAAAA CGCCTGCANT TGCNTTGGCA TACNTGTTTT TGGGTNAAG GCTATGAACT 720
GAATGAAAGG GCCCCNCTAC TGCNAAATTA NCCAACTTGC TCCCCNAAAT TTGGTGCTAT 780
AAAAANTGCC ACCNTTGATA TGCTTATNGG 810

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GGCAGGAGCT TGGCTGTAGT CTTCTTCTCA AGTAATCTTC GTCTTCTGA TTTGCTTGGT 60
TGGTGGTCGG TTGCAGGGCG AAGGGATGGG GATGGGGAGG CCGAGCGGAG CTGGTTCGAC 120
CCCGTGGTTG GTGGTGGTTC TTGTGCATTG GCTCCTCTGG GCCACCGAGA GGAGGCGAGG 180
GGCGGTGGTG GAGGCCTCCC ATGTGGAGTT TGCATCCCTC CAATCTGTTC CTGCCTCCGT 240
CGTCGACAAC AGGCTGAGGA CTGGGTATCA CTTCCAGCCC CCGAGGAACT GGATCAACGA 300
TCCAAATGGA CCCATGTACT TCAATGGCGT CTACCACCTC TTCTACCAGT ACAACCCCAA 360
TGGCTCCGTG TGGGGTAACA TCGTGTGGGC CCACTCGGTG TCGACCGACC TCGTCAACTG 420
GATAGCACTC GACCCGGCCA TCCGCCCCAG CAAGCCATTC CACATCAACG GATGCTGGTC 480
CGGCTCCGCC ACCGTCTCTC CCGGCAACAG GCCTGCGATC TTCTACACCG GCATCNACCC 540
CCANCANAAA CAACTGCANA ACNTTNCNTN CCCAAGGATC TGTCCAACCT TACTCCCCNA 600
NTGGGTCAAC CCCACTNCAA CCCCGTGATC CCCCTGGCGA CGCATCAACN CCACCCCTTC 660
CNCNAACCCN AATACGGNTT GGCGCNGTCC CNGCACCNC TGGAAACCCC TNGTNGGGAA 720
CNANTTGAAN CNGAAGGGGA AAGGCNTTCT TTNCCGAACA GGGAT 765

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 774 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GGCAGGAGCG GAGAANGCAA TCTCGCTCTC TCTCTACTGC ATCGCGGCTC TCGTCTCTGA 60

TTACTTGAGA TATGGCAGGA AAGGGCGAGG GGCCGGCGAT CGGGATCGAT CTCGGCACCA 120
CGTACTCGTG CGTCGGGGTG TGGCAGCACG ACCGGGTGGA GATCATCGCC AACGATCAGG 180
5 GGAATCGTAC CACCCCCTCC TATGTCGCCT TCACCGACTC CGAGCGCCTT ATCGGCGACG 240
CTGCCAAGAA CCAGGTCGCC ATGAACCCCA TCAACACCGT CTTTGATGCA AAGCGTTTAA 300
TTGGTAGGCG ATTCAGTGAT TCATCTGTCC AGAGTGACAT CAAGCTCTGG CCTTTCAAGG 360
10 TCATTCTGG TCCAGGTGAC AAGCCCATGA TTGTGTCCA ATACAAAGG GAGGATAAAC 420
AGTTTGCAGC TGAAGATATT TCTTCCATGG TTTTGATAAA GATGAAAGAA ATTGCTGAAC 480
15 CTACCTGGGG TCTGTTGTCA AGAATGCCGT CCTCACTGTT CCCGCTTACT TCAATGACTC 540
NCAACGCCCC GCCACAAAGG ATGCTGGTGT CATTGCTGGT CTCNATGTTA ATGANAATCA 600
TCAATGANCC CCCAGCACTG CTATTGCTTT ATGGCCTTGA CAAAANGCTA CTATTGTTGG 660
20 TGAATAAAAT TTCCTCATCT TCCATCTCCG GTGGGTGGCC TTTTGANTTC NCCTTCCTNA 720
CCATCCAAGA AGGTTTCTTT NAAGTCAAGG CCCTGCTGGT GANACCCANC TTGG 774

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: U-U125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGCAGGAGCT AGTCTCGAGT TTTTTTTTTT TTTTTTTTAA AATTGAAATT AGATGCGATT 60
45 TCGAATAGCA AACATAGTTC AGGATAAACC AACAACATTG TACCGAATTC GATAAGCTTA 120
GGAAACTAAA TTGCGTAAAC GAAACACTTG CATGAAAGCC TATATAATAT AAGGCCGACT 180
50 AGGGACNAAA TAACTTAATC GACCTCCTCG ATCTTTGGAC CAGCGCCGCT GCCACCAGCA 240
GGAGGAGCAT CATCATCCAT ACCACCAGCC ATGTCAGCAC CTGCTCCCTG GTACATCTTG 300
GCGATGATGG GATTGCATAT GCTCTCCAGC TCCTTCATCT TGTCATCGAA CTCGTCGGCT 360
55 TCTGCCAACT GGTGCCATC GAGCCATTGG ATGGCCTGCT CGATCGCATC CTCCGATCTT 420
CTTCTGTGCA GCAGCAGCAA GCTTGGAGGC AATCTTGTCG TCGTTAATGG TGTTCTCAT 480
GTTGTNAGCA TANTTTTCCA GANCATTCTT CCGATTCCAC CTCCTTTTTT ATGCTCCTCC 540
60 ATCTTCCTGA CTGTGTACTT CTCCGCTTCC CTGCACCATT TTCTCAATCT CCTCCTGCT 600
GACCTACCTT GTCCTTGGTG AAGGTGATCT TGTTCTCTGT CCAGTGGTCT NTCNTCNGCA 660
65 GAAANATTCC AGAATACCAT TGGGGTTCCA AATGTTNCAA AACCAAACCC GGTGGATTCT 720
TGAAGGAAAC CCCCCCTAA GGGCCCCAGG GTGGGAAATC CCCCCAAAA ACCCCCAAAT 780
TTTCCC 786

(2) INFORMATION FOR SEQ ID NO: 27:

- 35 -

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
(B) CLONE: U-U105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GGCACGAGCG AGTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTCAACAG GNAACCATAG 60
ACATTACACC AAACATAGAT GTCAACAATA CATGCCAAGC ATACCATTGC TTATTCCTTC 120
AGACCTCCGA TAGGACTTCC ACGCACACCA ACAGAGAGAA CTAAGACAGC AAAGCAGCGG 180
ACACATACAG CCCAAAAGGG TNNGTGACCC CCGCGGAGGN GGAGCNCCAG GTGAAGGGTG 240
GATTCCCTCT GAATGTTGTA TTCTGNCAGG GTGCGCCCGT CCTCNNTTTG NTTCCNTCT 300
NANATCNCCC NCTGNTGATC TGGTGGNAAT CCCCCCTTG TCCTGTGATT CTTGCTCTTG 360
ACNTTTTTCT CCCNTGTCNN ANCTCTCTNC CTNCTCTGGG TNTTGGGTCT TCCCCTGTTG 420
NANCNNTCTN TTNNCNTATC ATCTTGTNCT CCNCCNCCN CNCCTNTCNT TTCCTCNNNN 480
GGTNNA 486

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
(B) CLONE: U-U116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GGCACGAGTG ACAATGTCAA GGCCAAGATT CAGGATAAGG AGGGCATTCC CCCCACCAG 60
CAGAGGCTCA TCTTGCCGG CAAGCAGCTC GAGGATGGCC GCACCTTGGC TGATTACAAC 120
ATCCAGAAGG AGTCCACCCT CCACCTTGTC CTCCGCCTCC GTGGTGGCAT GCAAATCTTC 180
GTCAAGACTT TGA CTGGGAA GACCATCACC CTTGAGGTGG ANAGCTCGGA CACCATCGAC 240
AATGTAAAGG CCAAGATTCA GGACAAGGAG GGTNTTCCCC CGGACCAGCA AAGGCTCATC 300
TTTGCCGGCA AGCAGCTTGA GGATGGCCGC ACCCTGGCAG ATTACAACAT TCAGAAGGAG 360
TCTACCCTTC ACCTTGCTGCT GANACTTAGG GGTGGCATGC ANATCTTTGT TAAGACNCTC 420
NCAGGGGAAG ACCATTACCT TGGAGGTGGA NANCTCNGAC ACGATTGATA ATGTCNAGGC 480
AAAGATCCAN GACAAGGANG GGATTCCACC GGATCAGCAN ANGCTGATCT TTGCTGGGAA 540